AU 1812

INPUT SET: S6937.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
1                                    SEQUENCE LISTING
2
3    (1)      General Information:
4
5         (i) APPLICANT: Adams, Craig W.
6                        Pang, Patty P.-Y.
7                        Belei, Marina
8
9        (ii) TITLE OF INVENTION: Recombinant DNase B Derived from
10               Streptococcus pyogenes
11
12      (iii) NUMBER OF SEQUENCES: 16
13
14       (iv) CORRESPONDENCE ADDRESS:
15            (A) ADDRESSEE: Sheldon & Mak
16            (B) STREET: 225 South Lake Avenue, Ninth Floor
17            (C) CITY: Pasadena
18            (D) STATE: California
19            (E) COUNTRY: USA
20            (F) ZIP: 91001
21
22        (v) COMPUTER READABLE FORM:
23            (A) MEDIUM TYPE: Floppy disk
24            (B) COMPUTER: IBM PC compatible
25            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28      (vi) CURRENT APPLICATION DATA:
29            (A) APPLICATION NUMBER: US 08/482,785
30            (B) FILING DATE: 07-JUN-1995
31            (C) CLASSIFICATION: 435
32
33     (vii) PRIOR APPLICATION DATA:
34            (A) APPLICATION NUMBER: US/08/393,889
35            (B) FILING DATE: 24-FEB-1995
36
37            (A) APPLICATION NUMBER: US/08/082,845
38            (B) FILING DATE:
39
40    (viii) ATTORNEY/AGENT INFORMATION:
41            (A) NAME: Farber, Michael B.
42            (B) REGISTRATION NUMBER: 32,612
43            (C) REFERENCE/DOCKET NUMBER: 9521
44
45      (ix) TELECOMMUNICATION INFORMATION:
46            (A) TELEPHONE: (818) 796-4000
```

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/482,785*

INPUT SET: S6937.raw

```
47              (B) TELEFAX: (818) 795-6321
48
49
50  (2) INFORMATION FOR SEQ ID NO:1:
51
52          (i) SEQUENCE CHARACTERISTICS:
53              (A) LENGTH: 43 amino acids
54              (B) TYPE: amino acid
55              (D) TOPOLOGY: linear
56
57         (ii) MOLECULE TYPE: peptide
58
59        (iii) HYPOTHETICAL: NO
60
61          (v) FRAGMENT TYPE: N-terminal
62
63         (vi) ORIGINAL SOURCE:
64              (A) ORGANISM: Streptococcus pyogenes
65
66
67         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69         Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys Arg Leu
70         1               5                   10                  15
71
72
73         Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala Val Thr
74                     20                  25                  30
75
76
77         Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg
78                     35                  40
79
80  (2) INFORMATION FOR SEQ ID NO:2:
81
82          (i) SEQUENCE CHARACTERISTICS:
83              (A) LENGTH: 41 base pairs
84              (B) TYPE: nucleic acid
85              (C) STRANDEDNESS: single
86              (D) TOPOLOGY: linear
87
88         (ii) MOLECULE TYPE: DNA (genomic)
89
90        (iii) HYPOTHETICAL: NO
91
92         (iv) ANTI-SENSE: NO
93
94         (vi) ORIGINAL SOURCE:
95              (A) ORGANISM: Synthetic DNA primer
96
97
98         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
99
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INPUT SET: S6937.raw

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100   TAACGGATCC GAATCTACTT GGATCAAGAC GGGTTTTTTC T              41
101
102   (2) INFORMATION FOR SEQ ID NO:3:
103
104       (i) SEQUENCE CHARACTERISTICS:
105           (A) LENGTH: 41 base pairs
106           (B) TYPE: nucleic acid
107           (C) STRANDEDNESS: single
108           (D) TOPOLOGY: linear
109
110       (ii) MOLECULE TYPE: DNA (genomic)
111
112      (iii) HYPOTHETICAL: NO
113
114       (iv) ANTI-SENSE: NO
115
116       (vi) ORIGINAL SOURCE:
117           (A) ORGANISM: Synthetic DNA primer
118
119
120       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
121
122   CCGGGTCGAC CCGGGGAATG ACGGCAATCA TTGCTTTTTC T              41
123
124   (2) INFORMATION FOR SEQ ID NO:4:
125
126       (i) SEQUENCE CHARACTERISTICS:
127           (A) LENGTH: 23 amino acids
128           (B) TYPE: amino acid
129           (D) TOPOLOGY: linear
130
131       (ii) MOLECULE TYPE: peptide
132
133      (iii) HYPOTHETICAL: NO
134
135       (v) FRAGMENT TYPE: N-terminal
136
137       (vi) ORIGINAL SOURCE:
138           (A) ORGANISM: Streptococcus pyogenes
139
140
141       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
142
143       Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Xaa
144       1               5                   10                  15
145
146
147       Tyr Leu Asn Glu Ala Leu Ala
148                   20
149
150   (2) INFORMATION FOR SEQ ID NO:5:
151
152       (i) SEQUENCE CHARACTERISTICS:
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153              (A) LENGTH: 22 base pairs
154              (B) TYPE: nucleic acid
155              (C) STRANDEDNESS: single
156              (D) TOPOLOGY: linear
157
158         (ii) MOLECULE TYPE: DNA (genomic)
159
160        (iii) HYPOTHETICAL: NO
161
162         (iv) ANTI-SENSE: NO
163
164         (vi) ORIGINAL SOURCE:
165              (A) ORGANISM: Synthetic probe
166
167
168         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
169
170   CAUACNCART NWSNAAYGAY GT                              22
171
172
173   (2) INFORMATION FOR SEQ ID NO:6:
174
175          (i) SEQUENCE CHARACTERISTICS:
176              (A) LENGTH: 38 amino acids
177              (B) TYPE: amino acid
178              (D) TOPOLOGY: linear
179
180         (ii) MOLECULE TYPE: peptide
181
182        (iii) HYPOTHETICAL: NO
183
184          (v) FRAGMENT TYPE: N-terminal
185
186         (vi) ORIGINAL SOURCE:
187              (A) ORGANISM: Streptococcus pyogenes
188
189
190
191         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
192
193      Arg Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser
194       1               5                  10                  15
195
196
197      Lys Tyr Leu Asn Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn
198               20                  25                  30
199
200
201      Tyr Tyr Lys Thr Leu Gly
202               35
203
204   (2) INFORMATION FOR SEQ ID NO:7:
205
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206        (i) SEQUENCE CHARACTERISTICS:
207            (A) LENGTH: 1083 base pairs
208            (B) TYPE: nucleic acid
209            (C) STRANDEDNESS: double
210            (D) TOPOLOGY: linear
211
212       (ii) MOLECULE TYPE: DNA (genomic)
213
214      (iii) HYPOTHETICAL: NO
215
216       (iv) ANTI-SENSE: NO
217
218       (vi) ORIGINAL SOURCE:
219            (A) ORGANISM: Streptococcus pyogenes
220
221       (ix) FEATURE:
222            (A) NAME/KEY: CDS
223            (B) LOCATION: 129..944
224
225
226       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
227
228  GACAACGCCT TCTTTTTTCT CCTTACTATC TCCTTTAATT TTCATATTTT TTAAAAAAAC     60
229
230  TATTGATAAA CTAGTTAAGT AAGCGTATAC TATGGTTAGT TAGCGAAATT AGAAAAGAGG    120
231
232  ACAAGCAT ATG AAT CTA CTT GGA TCA AGA CGG GTT TTT TCT AAA AAA TGT     170
233           Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys
234            1               5                  10

235
236  CGG CTA GTA AAA TTT TCA ATG GTA GCT CTT GTA TCA GCC ACA ATG GCT     218
237  Arg Leu Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala
238   15               20                  25                  30
239
240  GTA ACA ACA GTC ACA CTT GAA AAT ACT GCA CTG GCA CGA CAA ACA CAG     266
241  Val Thr Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg Gln Thr Gln
242                   35                  40                  45
243
244  GTC TCA AAT GAT GTT GTT CTA AAT GAT GGC GCA AGC AAG TAC CTA AAC     314
245  Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn
246                   50                  55                  60
247
248  GAA GCA TTA GCT TGG ACA TTC AAT GAC AGT CCT AAC TAT TAC AAA ACT     362
249  Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr
250              65                  70                  75
251
252  TTA GGT ACT AGT CAG ATT ACT CCA GCA CTC TTT CCT AAA GCA GGA GAT     410
253  Leu Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp
254          80                  85                  90
255
256  ATT CTC TAT AGC AAA TTA GAT GAG TTA GGA AGG ACG CGT ACT GCT AGA     458
257  Ile Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg
258   95                  100                 105                 110
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/482,785*

INPUT SET: S6937.raw

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